



Sequence Listing

<110> Ashkenazi, Avi J.
Gurney, Austin

<120> RTD Receptor

<130> P1129R1 (REVISED)

<140> US 09/114,844

<141> 1998-07-14

<150> US 60/056,974

<151> 1997-08-26

<160> 10

<210> 1

<211> 386

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 310

<223> unknown amino acid

<400> 1

Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
1 5 10 15

Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
20 25 30

Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
35 40 45

Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
50 55 60

Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
65 70 75

Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
80 85 90

Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
95 100 105

Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
110 115 120

Cys	Lys	Ser	Gly	Gln	Thr	Asn	Lys	Ser	Ser	Cys	Thr	Thr	Thr	Arg
				125					130					135
Asp	Thr	Val	Cys	Gln	Cys	Glu	Lys	Gly	Ser	Phe	Gln	Asp	Lys	Asn
				140					145					150
Ser	Pro	Glu	Met	Cys	Arg	Thr	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly
				155					160					165
Met	Val	Lys	Val	Ser	Asn	Cys	Thr	Pro	Arg	Ser	Asp	Ile	Lys	Cys
				170					175					180
Lys	Asn	Glu	Ser	Ala	Ala	Ser	Ser	Thr	Gly	Lys	Thr	Pro	Ala	Ala
				185					190					195
Glu	Glu	Thr	Val	Thr	Thr	Ile	Leu	Gly	Met	Leu	Ala	Ser	Pro	Tyr
				200					205					210
His	Tyr	Leu	Ile	Ile	Ile	Val	Val	Leu	Val	Ile	Ile	Leu	Ala	Val
				215					220					225
Val	Val	Val	Gly	Phe	Ser	Cys	Arg	Lys	Lys	Phe	Ile	Ser	Tyr	Leu
				230					235					240
Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Val	His
				245					250					255
Arg	Val	Leu	Phe	Arg	Arg	Arg	Ser	Cys	Pro	Ser	Arg	Val	Pro	Gly
				260					265					270
Ala	Glu	Asp	Asn	Ala	Arg	Asn	Glu	Thr	Leu	Ser	Asn	Arg	Tyr	Leu
				275					280					285
Gln	Pro	Thr	Gln	Val	Ser	Glu	Gln	Glu	Ile	Gln	Gly	Gln	Glu	Leu
				290					295					300
Ala	Glu	Leu	Thr	Gly	Val	Thr	Val	Glu	Xaa	Pro	Glu	Glu	Pro	Gln
				305					310					315
Arg	Leu	Leu	Glu	Gln	Ala	Glu	Ala	Glu	Gly	Cys	Gln	Arg	Arg	Arg
				320					325					330
Leu	Leu	Val	Pro	Val	Asn	Asp	Ala	Asp	Ser	Ala	Asp	Ile	Ser	Thr
				335					340					345
Leu	Leu	Asp	Ala	Ser	Ala	Thr	Leu	Glu	Glu	Gly	His	Ala	Lys	Glu
				350					355					360
Thr	Ile	Gln	Asp	Gln	Leu	Val	Gly	Ser	Glu	Lys	Leu	Phe	Tyr	Glu
				365					370					375

Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
380 385

<210> 2
<211> 2082
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1085
<223> unknown base

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ccaactgcac ctcggttcta tcgattgaat tccccgggga tcctctagag 50
atccctcgac ctcgaccac gcgtccggaa cctttgcacg cgcacaaact 100
acggggacga tttctgattg atttttggcg ctttcgatcc accctcctcc 150

cttctc atg gga ctt tgg gga caa agc gtc ccg acc gcc 189
Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
1 5 10

tcg agc gct cga gca ggg cgc tat cca gga gcc agg aca 228
Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
15 20

gcg tcg gga acc aga cca tgg ctc ctg gac ccc aag atc 267
Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
25 30 35

ctt aag ttc gtc gtc ttc atc gtc gcg gtt ctg ctg ccg 306
Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
40 45 50

gtc cgg gtt gac tct gcc acc atc ccc cgg cag gac gaa 345
Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu
55 60

gtt ccc cag cag aca gtg gcc cca cag caa cag agg cgc 384
Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg
65 70 75

agc ctc aag gag gag gag tgt cca gca gga tct cat aga 423
Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg
80 85

tca gaa tat act gga gcc tgt aac ccg tgc aca gag ggt 462
Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly

90	95	100	
gtg gat tac acc att gct tcc aac aat ttg cct tct tgc	501		
Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys			
105	110	115	
ctg cta tgt aca gtt tgt aaa tca ggt caa aca aat aaa	540		
Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys			
120	125		
agt tcc tgt acc acg acc aga gac acc gtg tgt cag tgt	579		
Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys			
130	135	140	
gaa aaa gga agc ttc cag gat aaa aac tcc cct gag atg	618		
Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met			
145	150		
tgc cgg acg tgt aga aca ggg tgt ccc aga ggg atg gtc	657		
Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val			
155	160	165	
aag gtc agt aat tgt acg ccc cgg agt gac atc aag tgc	696		
Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys			
170	175	180	
aaa aat gaa tca gct gcc agt tcc act ggg aaa acc cca	735		
Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro			
185	190		
gca gcg gag gag aca gtg acc acc atc ctg ggg atg ctt	774		
Ala Ala Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu			
195	200	205	
gcc tct ccc tat cac tac ctt atc atc ata gtg gtt tta	813		
Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu			
210	215		
gtc atc att tta gct gtg gtt gtg gtt ggc ttt tca tgt	852		
Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys			
220	225	230	
cgg aag aaa ttc att tct tac ctc aaa ggc atc tgc tca	891		
Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser			
235	240	245	
ggg ggt gga gga ggt ccc gaa cgt gtg cac aga gtc ctt	930		
Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu			
250	255		
ttc cgg cgg cgt tca tgt cct tca cga gtt cct ggg gcg	969		

Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala
 260 265 270

gag gac aat gcc cgc aac gag acc ctg agt aac aga tac 1008
 Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr
 275 280

ttg cag ccc acc cag gtc tct gag cag gaa atc caa ggt 1047
 Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly
 285 290 295

cag gag ctg gca gag cta aca ggt gtg act gta gag tyg 1086
 Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa
 300 305 310

cca gag gag cca cag cgt ctg ctg gaa cag gca gaa gct 1125
 Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala
 315 320

gaa ggg tgt cag agg agg agg ctg ctg gtt cca gtg aat 1164
 Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn
 325 330 335

gac gct gac tcc gct gac atc agc acc ttg ctg gat gcc 1203
 Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala
 340 345

tcg gca aca ctg gaa gaa gga cat gca aag gaa aca att 1242
 Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile
 350 355 360

cag gac caa ctg gtg ggc tcc gaa aag ctc ttt tat gaa 1281
 Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
 365 370 375

gaa gat gag gca ggc tct gct acg tcc tgc ctg tgaaaag 1320
 Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
 380 385 386

aatctcttca ggaaaccaga gcttccctca tttacctttt ctctacaaa 1370

gggaagcagc ctggaagaaa cagtccagta cttgacccat gcccacaaca 1420

actctactat ccaatatggg gcagcttacc aatgggtccta gaactttggt 1470

aacgcacttg gagtaatttt tatgaaatac tgcgtgtgat aagcaaacgg 1520

gagaaattta tatcagattc ttggctgcat agttatacga ttgtgtatta 1570

agggtcgttt taggccacat gcgggtggctc atgcctgtaa tcccagcact 1620

ttgataggct gaggcagggtg gattgcttga gctcgggagt ttgagaccag 1670
 cctcatcaac acagtgaac tccatctcaa tttaaaaaga aaaaaagtgg 1720
 ttttaggatg tcattctttg cagttcttca tcatgagaca agtctttttt 1770
 tctgcttctt atattgcaag ctccatctct actgggtgtg gcatttaatg 1820
 acatctaact acagatgccg cacagccaca atgctttgcc ttatagtttt 1870
 ttaactttag aacgggatta tcttggttatt acctgtattt tcagtttcgg 1920
 atatTTTTga cttaatgatg agattatcaa gacgtacccc tatgctaagt 1970
 catgagcata tggacttacg agggttcgac ttagagtttt gagctttaag 2020
 ataggattat tgggggctta ccccccacctt aattagaaga aacattttat 2070
 attgctttac ta 2082

<210> 3
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence is synthesized.

<400> 3
 cataaaagtt cctgcaccat gaccagagac acagtgtgtc agtgtaaaga 50

<210> 4
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence is synthesized.

<400> 4
 cttcaggaaa ccagagcttc cctc 24

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence is synthesized.

<400> 5

ttctcccggtt tgcttatcac acgc 24

<210> 6

<211> 191

<212> PRT

<213> Homo sapiens

<400> 6

Gly	Arg	Gly	Ala	Leu	Pro	Thr	Ser	Met	Gly	Gln	His	Gly	Pro	Ser
1				5					10				15	

Ala	Arg	Ala	Arg	Ala	Gly	Arg	Ala	Pro	Gly	Pro	Arg	Pro	Ala	Arg
				20					25				30	

Glu	Ala	Ser	Pro	Arg	Leu	Arg	Val	His	Lys	Thr	Phe	Lys	Phe	Val
				35					40				45	

Val	Val	Gly	Val	Leu	Leu	Gln	Val	Val	Pro	Ser	Ser	Ala	Ala	Thr
				50					55				60	

Ile	Lys	Leu	His	Asp	Gln	Ser	Ile	Gly	Thr	Gln	Gln	Trp	Glu	His
				65					70				75	

Ser	Pro	Leu	Gly	Glu	Leu	Cys	Pro	Pro	Gly	Ser	His	Arg	Ser	Glu
				80					85				90	

Arg	Pro	Gly	Ala	Cys	Asn	Arg	Cys	Thr	Glu	Gly	Val	Gly	Tyr	Thr
				95					100				105	

Asn	Ala	Ser	Asn	Asn	Leu	Phe	Ala	Cys	Leu	Pro	Cys	Thr	Ala	Cys
				110					115				120	

Lys	Ser	Asp	Glu	Glu	Glu	Arg	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn
				125					130				135	

Thr	Ala	Cys	Gln	Cys	Lys	Pro	Gly	Thr	Phe	Arg	Asn	Asp	Asn	Ser
				140					145				150	

Ala	Glu	Met	Cys	Arg	Lys	Cys	Ser	Thr	Gly	Cys	Pro	Arg	Gly	Met
				155					160				165	

Val	Lys	Val	Lys	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val
				170					175				180	

His	Lys	Glu	Ser	Gly	Asn	Gly	His	Asn	Ile	Trp				
				185					190					

<210> 7

<211> 193

<212> PRT

<213> Homo sapiens

<400> 7

Met	Glu	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg
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Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arg	Pro
				20					25					30

Gly	Leu	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val
				35					40					45

Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	Leu	Ile	Thr	Gln	Gln	Asp
				50					55					60

Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser
				65					70					75

Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp
				80					85					90

Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr
				95					100					105

His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp
				110					115					120

Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr
				125					130					135

Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro
				140					145					150

Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
				155					160					165

Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His
				170					175					180

Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala		
				185					190					

<210> 8

<211> 158

<212> PRT

<213> Homo sapiens

<400> 8

Met	Ala	Arg	Ile	Pro	Lys	Thr	Leu	Lys	Phe	Val	Val	Val	Ile	Val
1					5				10					15

Ala	Val	Leu	Leu	Pro	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	20		25		30
Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg					
	35		40		45
His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser					
	50		55		60
Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr					
	65		70		75
Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val					
	80		85		90
Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg					
	95		100		105
Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn					
	110		115		120
Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu					
	125		130		135
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val					
	140		145		150
Glu Glu Phe Gly Ala Asn Ala Thr					
	155				

<210> 9
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 9
 Gly Gly Asp Pro Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu
 1 5 10 15
 Gly Leu Leu Arg Gly Pro Gly Ala Glu Asp Asn Ala His Asn Glu
 20 25 30
 Ile Leu Ser Asn Ala Asp Ser Leu Ser Thr Phe Val Ser Glu Gln
 35 40 45
 Gln Met Glu Ser Gln Glu Pro Ala Asp Leu Thr Gly Val Thr Val
 50 55 60
 Gln Ser Pro Gly Glu Ala Gln Cys Leu Leu Gly Pro Ala Glu Ala
 65 70 75
 Glu Gly Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Gly Ala

80	85	90
Asp Pro Thr Glu Thr Leu Met Leu Phe	Phe Asp Lys Phe Ala Asn	
95	100	105
Ile Val Pro Phe Asp Ser Trp Asp Gln	Leu Met Arg Gln Leu Asp	
110	115	120
Leu Thr Lys Asn Glu Ile Asp Val Val	Arg Ala Gly Thr Ala Gly	
125	130	135
Pro Gly Asp Ala Leu Tyr Ala Met Leu	Met Lys Trp Val Asn Lys	
140	145	150
Thr Gly Arg Asn Ala Ser Ile His Thr	Leu Leu Asp Ala Leu Glu	
155	160	165
Arg Met Glu Glu Arg His Ala Lys Glu	Lys Ile Gln Asp Leu Leu	
170	175	180
Val Asp Ser Gly Lys Phe Ile Tyr Leu	Glu Asp Gly Thr Gly Ser	
185	190	195
Ala Val Ser Leu Glu		
200		

<210> 10
 <211> 202
 <212> PRT
 <213> Homo sapiens

<400> 10
 Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
 1 5 10 15

Asp Pro Glu Arg Val Asp Arg Ser Ser	Gln Arg Pro Gly Ala Glu
20	25 30
Asp Asn Val Leu Asn Glu Ile Val Ser	Ile Leu Gln Pro Thr Gln
35	40 45
Val Pro Glu Gln Glu Met Glu Val Gln	Glu Pro Ala Glu Pro Thr
50	55 60
Gly Val Asn Met Leu Ser Pro Gly Glu	Ser Glu His Leu Leu Glu
65	70 75
Pro Ala Glu Ala Glu Arg Ser Gln Arg	Arg Arg Leu Leu Val Pro
80	85 90
Ala Asn Glu Gly Asp Pro Thr Glu Thr	Leu Arg Gln Cys Phe Asp

	95		100		105
Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met					
	110		115		120
Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala					
	125		130		135
Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys					
	140		145		150
Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu					
	155		160		165
Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile					
	170		175		180
Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly					
	185		190		195
Asn Ala Asp Ser Ala Leu Ser					
	200				

See
C1
cont